

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 17, 2003, 18:30:00 ; Search time 74.295 Seconds

(without alignment)
8745.081 Million cell updates/sec

Title: US-10-026-106E-9

Perfect score: 1472

Sequence: 1 aagggccatgscgsggcccga.....acatccaccgaatcgtatg 1472

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 569978 seqs, 22069156 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents NA.*
1: /cgn2_6/prodata/2/ina/5A COMB.seq.*
2: /cgn2_6/prodata/2/ina/5B COMB.seq.*
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4: /cgn2_6/prodata/2/ina/6B COMB.seq.*
5: /cgn2_6/prodata/2/ina/PCtUS COMB.seq.*
6: /cgn2_6/prodata/2/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	42.2	2.9	971	4 US-09-535-008-39	Sequence 39, Appl
C 2	42.2	2.9	7218	1 US-08-232-463-14	Sequence 14, Appl
C 3	39.6	2.7	2751	4 US-09-252-991A-14671	Sequence 14671, A
C 4	39.6	2.7	3201	4 US-09-252-991A-14959	Sequence 14959, A
C 5	39.6	2.7	3402	4 US-09-252-991A-14791	Sequence 14791, A
C 6	39.2	2.7	1678	4 US-08-650-766-2	Sequence 2, Appl
C 7	39.2	2.7	1678	4 US-08-650-766-2	Sequence 2, Appl
C 8	39.2	2.7	1954	3 US-08-922-635-2	Sequence 2, Appl
C 9	39.2	2.7	3318	3 US-08-922-635-3	Sequence 3, Appl
C 10	39.2	2.7	3318	3 US-08-922-635-3	Sequence 3, Appl
C 11	39.2	2.7	3318	3 US-08-922-635-3	Sequence 3, Appl
C 12	39.2	2.7	3385	3 US-08-650-766-1	Sequence 1, Appl
C 13	39.2	2.7	3385	3 US-08-922-635-1	Sequence 1, Appl
C 14	39.2	2.7	3385	3 US-08-922-635-1	Sequence 1, Appl
C 15	39.2	2.7	5128	4 US-09-389-487-1	Sequence 1, Appl
C 16	39.2	2.7	5128	4 US-09-389-487-1	Sequence 1, Appl
C 17	39.2	2.7	15202	3 US-08-922-635-21	Sequence 21, Appl
C 18	39.2	2.6	2900	2 US-09-027-337-9	Sequence 9, Appl
C 19	39.2	2.6	2900	2 US-09-027-337-9	Sequence 9, Appl
C 20	39.2	2.6	3147	2 US-09-027-337-1	Sequence 1, Appl
C 21	39.2	2.6	3147	2 US-09-027-337-1	Sequence 1, Appl
C 22	39.2	2.6	3147	2 US-09-027-337-1	Sequence 1, Appl
C 23	39.2	2.6	2168	1 US-07-865-662F-10	Sequence 10, Appl
C 24	39.2	2.6	2168	1 US-07-865-662F-10	Sequence 10, Appl
C 25	37.6	2.5	7892	2 US-07-916-098A-40	Sequence 40, Appl
C 26	37.6	2.5	1422	4 US-08-979-608A-13	Sequence 13, Appl
C 27	35.8	2.4	1617	4 US-08-979-608A-11	Sequence 11, Appl
C 28	35.8	2.4	4195	1 US-08-340-011-1	Sequence 1, Appl

28	35.8	2.4	4195	3 US-08-301-710-1	Sequence 1, Appl
29	35.8	2.4	4416	3 US-08-795-430-1	Sequence 1, Appl
30	35.8	2.4	4416	4 US-09-355-700-1	Sequence 1, Appl
31	35.8	2.4	4416	4 US-08-601-132-36	Sequence 36, Appl
32	35.8	2.4	4425	1 US-08-222-616-31	Sequence 31, Appl
33	35.8	2.4	4425	4 US-08-446-648-31	Sequence 31, Appl
34	35.8	2.4	4425	5 PCT-US95-04228-31	Sequence 31, Appl
35	35.8	2.4	4795	3 US-08-340-011-3	Sequence 3, Appl
36	35.8	2.4	4795	3 US-08-301-710-3	Sequence 3, Appl
37	35.8	2.4	9108	4 US-08-446-648-45	Sequence 45, Appl
38	35.8	2.4	9108	5 PCT-US95-04228-45	Sequence 45, Appl
39	35.6	2.4	1151	4 US-07-852-132A-15	Sequence 15, Appl
40	35.6	2.4	1151	1 US-08-086-439C-2	Sequence 2, Appl
41	35.6	2.4	1151	1 US-08-434-877-2	Sequence 2, Appl
42	35.6	2.4	1367	3 US-08-475-742-3	Sequence 3, Appl
43	35.6	2.4	1367	4 US-08-261-293-3	Sequence 3, Appl
44	35.6	2.4	1370	1 US-08-056-051-1	Sequence 1, Appl
45	35.6	2.4	1370	1 US-07-928-611-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1
US-09-535-008-39/C
Sequence 39, Application US/09535008
Patent No. 6465629
GENERAL INFORMATION:
APPLICANT: Wong, Alexander K.C.
APPLICANT: Teng, David H.-F.
TITLE OF INVENTION: BRN1 IS A TUMOR SUPPRESSOR THAT IS MUTATED IN PROSTATE
FILE REFERENCE: 2318-259
CURRENT APPLICATION NUMBER: US/09/535,008
CURRENT FILING DATE: 2000-03-23
EARLIER APPLICATION NUMBER: U.S. 60/125,806
EARLIER FILING DATE: 1999-03-23
NUMBER OF SEQ ID NOS: 77
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 39
LENGTH: 971
TYPE: DNA
ORGANISM: Homo sapiens
US-09-535-008-39

Query Match 2.9%; Score 42.2; DB 4; Length 971;
Best Local Similarity 49.3%; Pred. No. 0.078;
Matches 110; Conservative 0; Mismatches 113; Indels 0; Gaps 0;

QY	1044	GCTGGGCGAGCACTGTGAGCTCTCCGCGAGAGGCTGGGCTCTGCGTATTGCGT	1103
DB	831	GATGAGACAGCTCTTAAGACACCACTTCGCGAGGCTGGGCTCTGCTGCTGCTGCTG	772
QY	1104	AGAGGGGCGAGGCGAGGCGCGGGTGGGATGGGCACCGAGAACTCTCCACCACTTG	1163
DB	771	ACAGATGCGCCAGCGAGGCGAGGAGCGGTCAACACAGCGGTGAGTCACTGCGCAG	712
QY	1164	AATTCCTCCAGAGCTCGGGTTTCCTGGAAGAGCTCCGAGAAATTAACCTGCTGCGG	1223
DB	711	TGGGACATGAGAGCTTGAAGAGCAGAGAAATCACTTACTCTCTCTCTCTCTGAG	652
QY	1224	CAACTCTGGGCGACCTTACACCGGAGCCCAATCTGCTGCTG	1266
DB	651	CCACTTCTTCACTATCAAGACTTCGAGAGCTACTTCACTACTG	609

RESULT 2
US-08-232-463-14/C
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DONNER, F.

APPLICANT: SCHEIFLINGER, F.
 APPLICANT: FALKNER, F. G.
 TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
 NUMBER OF SEQUENCES: 52
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Foley & Larnier
 STREET: 1800 Diagonal Road, Suite 500
 CITY: Alexandria
 STATE: VA
 COUNTRY: USA
 ZIP: 22113-0299
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/232,463
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/07/935,313
 FILING DATE:
 APPLICATION NUMBER: EP 91 114 300.6
 FILING DATE: 26-AUG-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: BENT, Stephen A.
 REGISTRATION NUMBER: 29,768
 REFERENCE/DOCKET NUMBER: 30472/114, 1MMU
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 836-9300
 TELEFAX: (703) 683-4109
 TELEX: 899149
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 7218 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 CLONE: PTZpt-F1s
 US-08-232-463-14

Query Match 2.9%, Score 42.2, DB 1, Length 7218;
 Best Local Similarity 4.9%, Pred. No. 0.17, Mismatches 176, Indels 0, Gaps 0;
 Matches 20, Conservative 210, Mismatches 176, Indels 0, Gaps 0;
 760 AAGAGACTGACAGAGGCTGACGCGCTGAGTCAAGGCGCCAGCCAGCCAGCA 819
 1449 AAGAGATTGGTACRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1390
 820 GACAAAGATGAGAGAGCCTTGACAGAGCAAGAGAGAGATGAGAGACACAGA 879
 1389 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1330
 880 AGATGCGCTGACCTTCAGCTTACATGACCACTTCTTCTGCGGCAAGACAGA 939
 1329 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1270
 940 GGCTCAGGAGCACTCGAGGCT?TGTGGTGAGACTCAGGAGGCGCCAGGCTCTCT 999
 1269 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1210
 1000 GGTCCAGAGGAGCTCTCTGCTGGAGTTCTTCAAGACAGAGCTGGGCAAGCTGT 1059
 1209 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1150
 1060 GGACTCTCTGAGCAGAGGCTGGGCTCTGAGCTATTGGTGAGAGGAGGAGCCCA 1119
 1149 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1090
 1120 AGGCGGAGTGGGAGTGGGACCAAGATCTTCCACACACTGAA 1165

Db 1089 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1044
 RESULT 3
 US-09-252-991A-14671
 Sequence 14671, Application US/09252991A
 Patent No. 6551795
 GENERAL INFORMATION:
 APPLICANT: Marc J. Rubenfield et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 FILE REFERENCE: 107196.136
 CURRENT APPLICATION NUMBER: US/09/252,991A
 PRIOR FILING DATE: 1999-02-18
 PRIOR APPLICATION NUMBER: US 60/074,788
 PRIOR FILING DATE: 1998-02-18
 PRIOR APPLICATION NUMBER: US 60/094,190
 NUMBER OF SEQ ID NOS: 33142
 SEQ ID NO 14671
 LENGTH: 2751
 TYPE: DNA
 ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-14671

Query Match 2.7%, Score 39.6, DB 4, Length 2751;
 Best Local Similarity 54.9%, Pred. No. 0.58, Mismatches 64, Indels 0, Gaps 0;
 Matches 78, Conservative 0, Mismatches 64, Indels 0, Gaps 0;
 380 CGGCCCCACCTGTCTGTGTCTGATCCAGAGAGAGATCTGTAGTCCATGCCAGT 439
 438 CGGACATCGCATCATGTCTCTCACTGACCTCGAGAGACCCAGATGCGCGGAGATGT 497
 440 ACCAGCTGCCCCCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 499
 498 AGAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 557
 500 AGGGGGCGGAAACAGACCTT 521
 558 TGAGCATGCGCGGAGCTGCT 579

RESULT 4
 US-09-252-991A-14959/c
 Sequence 14959, Application US/09252991A
 Patent No. 6551795
 GENERAL INFORMATION:
 APPLICANT: Marc J. Rubenfield et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 FILE REFERENCE: 107196.136
 CURRENT APPLICATION NUMBER: US/09/252,991A
 PRIOR FILING DATE: 1999-02-18
 PRIOR APPLICATION NUMBER: US 60/074,788
 PRIOR FILING DATE: 1998-02-18
 PRIOR APPLICATION NUMBER: US 60/094,190
 NUMBER OF SEQ ID NOS: 33142
 SEQ ID NO 14959
 LENGTH: 3201
 TYPE: DNA
 ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-14959
 Query Match 2.7%, Score 39.6, DB 4, Length 3201;
 Best Local Similarity 54.9%, Pred. No. 0.62, Mismatches 64, Indels 0, Gaps 0;
 Matches 78, Conservative 0, Mismatches 64, Indels 0, Gaps 0;
 380 CGGCCCCACCTGTCTGTGTCTGATCCAGAGAGAGATCTGTAGTCCATGCCAGT 439
 2702 CGGACATCGCATCATGTCTCTCACTGACCTCGAGAGACCCAGATGCGCGGAGATGT 2643
 440 ACCAGCTGCCCCCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 499

Mon Sep 22 11:34:33 2003

us-10-026-106 -9.rn1

Page 4

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; SEQ ID NO 2
; LENGTH: 1954
; TYPE: DNA
; ORGANISM: Homo sapiens
us-08-922-635-2

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Query Match	2.74	Score 39.2	DB 3	Length 1954
Best Local Similarity	54.84	Pred. No. 0.65		
Matches 74, Conservative	0	Mismatches 61	Indels 0	Gaps 0

Accession	Sequence	Position
Oy	84 TCCACAGGACCAACAGGAGGATGAGGAGGACACAGAAAGATGGGCTCAGC	500
Oy	663 TACACAGGCGAGGAGGATGACGAGGAGGAGGAGAGAGAGAGTGTGAGAACCG	722
Db	901 CTAACATTAACACACTTTCTTCTCGGCGAAGAGCAACAGGCTCCAGGCACTCGGAGC	960
Oy	723 CTACTTTAAATGGGCGCCCAACGTCGAGAGAGAGAGAGAGAGGCTCAAGGGAGAGA	782

QY 961 ? ? ? T G T G G G T G A 975
| | | | |
Db 783 A G A G A G A G A G A G A 797

RESULT 9
US-08-650-766-3

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: Sequence 3 Application US/08650766D
:
: Patent No. 6015690
:
: GENERAL INFORMATION:
:
: APPLICANT: PILETZ, John E.
: APPLICANT: IVANOV, Tina R.
: TITLE OF INVENTION: DNA SEQUENCE ENCODING A HUMAN IMIDAZOLINE RECEPTOR AND
: TITLE OF INVENTION: METHOD FOR CLOWING THE SAME
:

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Patent No. 6015690

; CURRENT APPLICATION NUMBER: US/08/650,766
 ; CURRENT FILING DATE: 1996-05-20
 ; EARLIER APPLICATION NUMBER: US 60/012,600

NUMBER OF SEQ ID NOS: 21

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; SOFTWARE: Pat
; SEQ ID NO 3
; LENGTH: 3318

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ORGANISM: Homo sapiens
US-08-650-766-3

Query Match	2.7%	Score 39.2	DB 3	Length 3318
Best Local Similarity	54.8%	Pred. NO. 0.8		
Matches 74; Conservative	0	Mismatches 61	Indels 0	Gaps 0

Dy 841 TGCAGAGGACGAAGAAGAGAGATGAGAGGACACAGAAATTGGCTTCACTCCACC 900
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2027 TGAACAGGGCGAGAGAGGATGAGAGAGAGAGGAAGAAGAGAGCAGTGACTTGAAACCG 208

Oy 901 CTACATGAACCACTTCTTTCCTGGGGCAAGCACCAAGCTCCAGGGCACTCGAGAGC 960
 |||||
 Db 2087 CTACTTTGAAATGGGGCCCCCAGACTGTGAGGAGGAGAGGAGGAGGCCAGGGGGAGGA 2146

Qy	961	??TGGTGGGTGA	975
Db	2147	AGAGGAGGAGGA	2161

RESULT 10
US-08-922-635-3
Generation 3 Analysis of the ITS/08022635A

Sequence 3, Application US/0892463A
Patent No. 603871
GENERAL INFORMATION: John E.
APPLICANT: PILSTZ, Tina R.
TITLE OF INVENTION: DNA MOLECULES ENCODING IMIDALINE RECEPTIVE POLYPEPTIDES
TITLE OF INVENTION: AND POLYPEPTIDES ENCODED THEREBY
FILE REFERENCE: Corrected Sequence Listing

Patent No. 6033871
CURRENT APPLICATION NUMBER: US/08/922,635A

1 CURRENT FILING DATE: 1997-09-03
2
3 EARLIER APPLICATION NUMBER: 08/650,766
4
5 EARLIER FILING DATE: 1996-05-20
6
7 EARLIER APPLICATION NUMBER: 60/012,600
8
9 EARLIER FILING DATE: 1996-03-01
10

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; NUMBER OF SEQ ID NOS: 22
;
; SOFTWARE: Patentin Ver. 2.0
;

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; SEQ ID NO 3
; LENGTH: 3318
; TYPE: DNA

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; TYPE: DNA
; ORGANISM: Homo sapiens
HE-08-922-635-3

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US-08-922-635-3

Query Match	Score	DB 3	Length
2.74%	39.21		3318
54.94%	0.81		

Best Local Similarity 54.8%; Pred. NO. 0.8;
Matches 74; Conservative 0; Mismatches 61; Indels 0; Gaps 0

Qy 8+1 TCGAGGAGCCAGAGGAGGATGTAGAGAGACACAAAGTGGCTTTCTTCCTCCTCT
| | | | | | | | | | | | | | | | | | | |
Db 2027 TGAAACAGGCCAGAGGAGGATGAAGAGAGAGAGAGAAGTAGAGAGACTTGCTGAGAACCG 2086
| | | | | | | | | | | | | | | | | | | |

[illegible]

QY	961	??TGTGGGGTGA	9/5
Db	2147	AGAGGAGGAGA	2161

RESULT 11
US-09-389-487-3
US-09-389-487-3

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; sequence 3, application US/0938948A
; Patent No. 6576742
GENERAL INFORMATION:

```

GENERAL INFORMATION:
APPLICANT: PILETZ, John E.
APPLICANT: IVANOV, Tina R.

APPLICANT: YANOV, ILLIA N.
TITLE OF INVENTION: DNA SEQUENCE ENCODING A HUMAN IMIDAZOLINE RECEPTOR AND
TITLE OF INVENTION: METHOD FOR CLONING THE SAME

FILE OF INVENTION: CORRECTED SEQUENCE LISTING
FILE REFERENCE: Corrected Sequence Listing
Patent No. 6576742

CURRENT APPLICATION NUMBER: US/09/389,487
CURRENT FILING DATE: 1999-09-03

EARLIER APPLICATION NUMBER: US 08/650,766
EARLIER FILING DATE: 1996-05-20

NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn Ver. 2.0.0; SEQ ID NO 3
; LENGTH: 3318
;

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; TYPE: DNA
; ORGANISM: Homo sapiens

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US-09-389-487-3
 Date: March 27; Score 39.2; DB 4; Length 3318

Query Match	2.74	Score (5.24)	22.17
Best Local Similarity	54.81	Pred. No. 0.8	
Marches 74: Conservative	0	Mismatches	61
		Indels	0
		Gaps	0

Oy 841 TGCAGGACGAAAGAGAGATGAGAGACAAGAAGATGGCGTTCAGCTTCCAGCC 900
| | | | | | | | | | | | | | | | | |
2027 TGGAACAGGCGCAGAGAGCATGAGGAGAGCAAGAGACGCTGCGTTGAGAACCG 208

901 CTACATTGACCACTTTCTTTCCTGGGGCAGAAGCACCCAGGCGTCCAGGGGCCTTGGAAGGC 960
 |||||
 2087 CTACTTTTGAAATGCGGGCCCCCAACACTTGACAGAGAGAGAGAGAGGCCAAGGCGGGAGGGA 2146

QY 961 ??TGTGGGTGCA 975
| | | |
Db 2147 AGAGGAGGAGGAAGA 2161

RESULT 12

Query Match	2.74;	Score 39.2;	DB 3;	Length 3385;
Best Local Similarity	54.84;	Pred. No. 0.81;		
Matches 74;	Conservative	0;	Mismatches 61;	Indels 0;
			Gaps	0

RESULT 15
US-09-364-206-1
Sequence 1, Application US/09364206
Patent No. 6475752
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Tang, Y. Tom
APPLICANT: Baugh, Matthew R.
APPLICANT: Kaser, Matthew R.
TITLE OF INVENTION: Mammalian Imidazoline Receptor
FILE REFERENCES: PC-0006 US
CURRENT APPLICATION NUMBER: US/09/364, 206
CURRENT FILING DATE: 1999-07-30
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PERL Program
SEQ ID NO 1

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1  LENGTH: 5128
2  TYPE: DNA
3  ORGANISM: Homo sapiens
4  FEATURE:
5  NAME/KEY:
6  OTHER INFORMATION: 129581CB1
7  PUBLICATION INFORMATION:
US-09-364-206-1

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Query Match      2.7%; Score 39.2; DB 4; Length 5128;
Best Local Similarity 54.8%; Pred. No. 0.95;
Matches 74; Conservative 0; Mismatches 61; Indels 0; Gaps 0.

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QY 841 TCACAGGACGAAGAGAGAGAGATGAGAGAGACACAGAAATGCGCTCAGCTTCAGC 900
Db 1920 TGAACAGGCGGAGAGAGAGATGAGAGAGAGAAAGAGAGACGTGCTGAGAACCG 1979
QY 901 CTACCTTGACACACTTTCTTCTGGGCAAGACCCAGGCTCCAGGGCCTCTGGAGGC 960
Db 1980 CTACTTTGAATGGGCCCCCAGACGTGAGAGAGACAGGAGAGGCCAGGGGAGAGA 2039
QY 961 TTTGTGGGGGTGGA 975
Db 2040 AGAGAGGAGGAGAGA 2054

Search completed: September 17, 2003, 22:16:18
Job time : 75.295 secs